

EXHIBIT 2

[illegible][illegible]

```
# Aligned_sequences: 2
# 1: SEQ175
# 2: G_kausotophilus
# Matrix: EBL08LM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5

#
# Length: 553
# Identity:      252/553 (45.6%)
# Similarity:    252/553 (45.6%)
# Gaps:          119/553 (21.5%)
# Score: 1104.5
#
```

SEQ175	1	atgattaacgcgctc---attttggtggccagg-----ttaa	34
G_kausotphilu	1	ttaaaacggcaaatcatcatcagaatatcgatcgctggccgctcaattgg	50
SEQ175	35	cgaga-gatc----cggagtttcgcttaac----tccaagcgga----g	70
G_kausotphilu	51	cgaaggatcgttcacgtgcgggccaaccccttttctgttcggtatttg	100
SEQ175	71	tgg--ctg---ttgcacgctttacg-----ctcggctcaaccgtc-	106
G_kausotphilu	101	tggttctgattcttgc-cgaattgggaatgagcccatagt-agccgct	148
SEQ175	107	-cgtttacaaatcagcaggggcgagcggg---aaacggattttatcaatgt	153
G_kausotphilu	149	gctgtgcgcctc-gctgctcgtcgtctccttcggc--tcaagaaattg	195
SEQ175	154	gtcgtttggcgccgcga---ggcg-gaaaacgtcgccaactttttgaa	197
G_kausotphilu	196	gaagctatcgcgcacacttcctcagctacacg-cgcgcactctttga	244
SEQ175	198	aaaggggaacttgctgtg--tgctgatggcgactgcaaaaccgc--agc	243
G_kausotphilu	245	ttttcatagct--cgaggttcgactggccatcgac--accagccaagc	290
SEQ175	244	tatgaataacaagaggtcggcgt-gtgtcagctgacggaagtgtgtgctg	292
G_kausotphilu	291	tccctcttttcaaaagtctggcagcgttttc-cgac-----tggcgggc	334
SEQ175	293	atagcgtccaattctctga--cgaagaagacagcgagcagcgggggg	340
G_kausotphilu	335	caaacacacacttgaataaaatcogt--ccgcctgcgcctgc-tgatt	381
SEQ175	341	cgacagcaggcgct-actatggggtaccattccattcgggcaagatca	389
G_kausotphilu	382	tgtaaacgcagcaggttgacgcgag---cgttaaagct--ggcga---ca	421

SEQ175	330	gaacccccaatatccgaacagcaaaagggtttcgcgcctcgatgacgac	439
		
G_kausotphilu	422	g--ccac-----tcgcgttg-----gaggt-aaagcgaac--tcgcgat	455
SEQ175	440	ctttccccaatgacggcagccgcatgattctctgatagatgatttcgcg	489
		
G_kausotphilu	456	ctctcgttaa-----cctgcgcaccaaatgac-gcggttaat-----ca	494
SEQ175	490	ttt	492
G_kausotphilu	495	t	495

```

# Program: needle
# RunDate: Mon Jul 31 07:12:56 2006
# Align_format: srspair
# Report_file: /ebi/outserv/old-work/needle-20060731-0712551097974.output

```

```

#

```

```

# Aligned_sequences: 2
# 1: SEQ175
# 2: B_cereus
# Matrix: EBL0SUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 583
# Identity: 246/553 (44.5%)
# Similarity: 246/553 (44.5%)
# Gaps: 101/553 (18.3%)
# Score: 1047.0
#

```

```

#

```

```

SEQ175      1      atgattaaccg-cgtcattttggtcggcagggttaacgagagatcc      44
              |.|.|.|.| | | | | | | | | | | | | | | | | | | | | |
B_cereus    1      ttagaacggttaaatcgtcgtcggaatgtcgatcggttgac-ctacatt      49
              |.|.|.| | | | | | | | | | | | | | | | | | | | | |
SEQ175      45     ggaggtg---cgttacactcc---aaagcgagtggtc---gttgccacg      84
              |.|.| | | | | | | | | | | | | | | | | | | | | | | |
B_cereus    50     gaaatggatcgtcattcttcgttaaatccagagttaccttggtttacctga      99
              |.|.| | | | | | | | | | | | | | | | | | | | | | | |
SEQ175      85     tttaacgtcgcgggtcaaccg-----tcc---gtttacaacacgacagg      124
              | | | | | | | | | | | | | | | | | | | | | | | | | |
B_cereus    100    attactagattgaccaaatgggttagacgttggtttaccgaaac--cagc      147
              | | | | | | | | | | | | | | | | | | | | | | | | | |
SEQ175      125    gcgagcgggaaacggattttttatcaatgtgtcgtttggcgccca----      170
              |.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|
B_cereus    148    tcttgatggtgtgctgattaaatgaaccagttgctccccacgcattac      197
              |.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|
SEQ175      171    --ggcggaataacgtcgccaatttttgaanaaggggagccttggtcgt---      214
              | | | | | | | | | | | | | | | | | | | | | | | | | |
B_cereus    198    gcggtctaaaaattgcacgttttcgcaa----gaactt--ctgttac      240
              | | | | | | | | | | | | | | | | | | | | | | | | | |
SEQ175      215    gtgt---cgatggcgactgcgaaacccgcagctatgaaatcaagaaggt      261
              |.| | | | | | | | | | | | | | | | | | | | | | | | |
B_cereus    241    gtatacagtttaccattctgttcctcgttaattacaggtttgaaagcgc      290
              |.| | | | | | | | | | | | | | | | | | | | | | | | |
SEQ175      262    cggcgtgtgtacgtacggaagtggtggtgctgatacgtccaatttcttga      311
              |.| | | | | | | | | | | | | | | | | | | | | | | | |
B_cereus    291    catc----tac--gcctgctaagctaaccttttt---tcaataaatttgc      330
              | | | | | | | | | | | | | | | | | | | | | | | | | |
SEQ175      312    gccgaaaggaaacgagcgcagcagcgagggcgagaca-----gcagcggtc      355
              |.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|
B_cereus    331    tacgtttttctgctgttttaacgcacattac-acaattaataagtcagct      379
              |.| | | | | | | | | | | | | | | | | | | | | | | | |
SEQ175      356    actarggggatccattccatttcgggcaagatc-agaacccacaaatacc      404
              |.| | | | | | | | | | | | | | | | | | | | | | | | |
B_cereus    380    tcac--gtrccacttgctgatt--ggcaaatgcgcgattcacag-----c      420
              |.| | | | | | | | | | | | | | | | | | | | | | | | |

```

SEQ175	448	gaacgaaagaaaggtttggcgcgatcgatgacgacatcctttgcgaatgacg	454
B_cereus	421		
	421	taacgtaaaag----tagctactgc---gac-accat gggggtgtaacg	462
SEQ175	455	---gcacgcgatcgatattt-----ctgagtgatatttgcgcgatt	492
B_cereus	463		
	463	taagttag- -ggctccttagt taaacgaccaacgaggataaacagattcat	510
SEQ175	493	492	
B_cereus	511	caa	513

本文件由生物信息学中心提供，仅供科研使用，不得用于商业用途。##

Program: needle
RunDate: Mon Jul 31 07:14:27 2006
Align_format: srapair
Report_file: /ebi/extern/old-work/needle-20060731-0714262184817C.output
本文件由生物信息学中心提供，仅供科研使用，不得用于商业用途。##

本文件由生物信息学中心提供，仅供科研使用，不得用于商业用途。##

```
# Aligned_sequences: 2
# 1: SEQ175
# 2: B_anthraxis
# Matrix: EBI6SUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 577
# Identity: 237/577 (41.1%)
# Similarity: 237/577 (41.1%)
# Gaps: 131/577 (22.7%)
# Score: 1040.5
#
## 本文件由生物信息学中心提供，仅供科研使用，不得用于商业用途。##

SEQ175      1      atgattaaccg-cgtcattttggtcgccaggttaacgagagatcc      44
              |.|.|.|.| | | | | | | | | | | | | | | | | | |
B_anthraxis 1      ttgaacggcgttaaatcgctgcggaaatgtcgatcggttgac-ctacattt      49
              |.|.|.| | | | | | | | | | | | | | | | | | |
SEQ175      45     ggaggttg---cgttacactcc---aagcggagtggt---gttgccacg      84
              |.|.| | | | | | | | | | | | | | | | | | |
B_anthraxis 50     gaaaatggatcgctcattcttcgtaaatccagagtttcttgggtacattg      99
              |.|.| | | | | | | | | | | | | | | | | | |
SEQ175      85     tttaacg-----tcggcgtaacc-----gtcc---gtttacaa      115
              |.|.| | | | | | | | | | | | | | | | | | |
B_anthraxis 100    gttgccgaattactagattgaccaaatgggttagagctttggttaaccga      149
              |.|.| | | | | | | | | | | | | | | | | | |
SEQ175      116    atcagcagggggagcgggaaacggattttattcaatgtctgtttgggc      165
              |.| | | | | | | | | | | | | | | | | | | | |
B_anthraxis 150    aac--cagctcctgatgggtgctgattaaatgaaccagttgctcccccac      197
              |.| | | | | | | | | | | | | | | | | | | | |
SEQ175      166    cgcca-----ggcggaaacgtgcgcaacttttgaiaaaggaggagctt      209
              | | | | | | | | | | | | | | | | | | | | | |
B_anthraxis 198    cgcattacgcggctctaaaaattgtacgcttccggcaa-----gaactt      242
              | | | | | | | | | | | | | | | | | | | | | |
SEQ175      210    ggtcggtgtcgatgcccgaactgcaaacccgcagctatgaaatcaagaag      259
              | | | | | | | | | | | | | | | | | | | | | |
B_anthraxis 243    --ctgttacatacacgcgttaccattcttgcctcctgtaattacagagttt      290
              | | | | | | | | | | | | | | | | | | | | | |
SEQ175      260    gtcggcggtgtgtaactgacggaagtgggtggt-----gatagcg      298
              |.|.| | | | | | | | | | | | | | | | | | |
B_anthraxis 291    gaagacgtccatcatcgcgctgctgaagctacatttttttaataatttgc-      339
              |.|.| | | | | | | | | | | | | | | | | | |
SEQ175      299    tccaatctc-----ttgagccgaaaggaaacgagcga-----gcagcga      336
              |.|.| | | | | | | | | | | | | | | | | | |
B_anthraxis 340    tacgtttctgctgttttaocgcattattacacatttaataaagtcagctt      389
              |.| | | | | | | | | | | | | | | | | | | | |
SEQ175      337    gggggcgacagagggcggtactactatggggatccattccca---ttcgggga      383
              |.| | | | | | | | | | | | | | | | | | | | |
B_anthraxis 390    cagcg-tcactctgttgattcgccaaatgcgcgattccacagctaacgttaa      438
              |.| | | | | | | | | | | | | | | | | | | | |
```

SEQ175	384 ag---atcagaaccaccaatatcgg---aacgaaa--aagggt-----	418
B_anthraxis	439 agtagctactgcacacccattggggcgtgtaacgtaagtcagggtcccttag	488
SEQ175	419 ttggcgg--catcgatgacgatcc-tttcgccaatgacggccagccgatac	465
B_anthraxis	489 ttaaacgcaccacgaggataaacagattccatcaat--cgaaccac	531
SEQ175	466 gatattttctgatgatgatttgcggtt	492
B_anthraxis	532	531

```

# Program: needle
# Rundate: Mon Jul 31 07:15:58 2006
# Align_format: strepair
# Report_file: /ebi/extern/old-work/needle-20060731-0715585573420.output

```

```

#
# Aligned_sequences: 2
# 1: SEQ175
# 2: B_thuringiensis
# Matrix: ESLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 556
# Identity: 238/556 (42.8%)
# Similarity: 238/556 (42.6%)
# Gaps: 98/556 (17.6%)
# Score: 1029.5
#
#=====

```

SEQ175	1	atgattaacgc-cgtcattttgtcggaaggttaacgagagatcc	44
B_thuringiens	1	ttagaacggttaaatcgtcgtcggaatctcgatcggttgac-ctacattt	49
SEQ175	45	ggaggtt---cgttacactcc---aagcggagtggt---gttgccacg	84
B_thuringiens	50	gaaatggatcgtcattctctgtaaatccagagtttcttggttacactg	99
SEQ175	85	tttacgc-----tcggcggtcaacc-----gtcc---gtttacaa	115
B_thuringiens	100	gttgcccgaaattactagattgaccaaatgggttagagctttggttaccca	149
SEQ175	116	atcagcaggggcagcgggaaacggattttattcaatgtgtgtttgcgc	165
B_thuringiens	150	aac--cagctcctgatggttgctgatataatgaaccagttgctccerac	197
SEQ175	166	cgcca-----ggcgaaaaacgtcgccaacttttgaanaaggggagctt	209
B_thuringiens	198	cgccattacggcggtctctaaaaattgtacgctttccgcaa-----gaactt	242
SEQ175	210	ggctgggtgtcgatggcgactgcaaaccccgagctatgaaatacaagag	259
B_thuringiens	243	--ctgttacataacacgcttaccatcttgcctcctgtaattacagagtt	290
SEQ175	260	gtcgccgtgtgtacgtgacggnaagtggtggtgatagcgtccaaattctt	309
B_thuringiens	291	gaagcgtccatctacgcgtgctaaagctacccctttt---tcaataattt	337
SEQ175	310	gagccgaagggaacgagcagcagcagcagcagcagcagcagcagcagcagc	353
B_thuringiens	338	gctacgttttctgctgttttacgcatattac-acaattataaagtcag	386
SEQ175	354	ctactatggggatccattccattcgggcaagatcagaaccaccaattac	403
B_thuringiens	387	cttcac--ggtcacctgttgattcg-----caaatcgcgattcac	426

SEQ175	404	---ggaacgaaaaagggtttggccgcacgatgatgacgacgtcctttgcgcataa	451
R_thuringiens	427	agctaacgcttaaaag---tagctaacgc---aac-accatctggggctgta	468
SEQ175	452	acg---gcacagcgatcgatattt-----ctgatgatgatttgcgcatt	492
R_thuringiens	469	acgttaaaatcag---ggtcctttagttaaagcaccacaggataaacacgatt	516
SEQ175	493		492
R_thuringiens	517	catcaa	522

```

# Program: needle
# Run date: Mon Jul 31 07:18:04 2006
# Align format: arspair
# Report file: /ebi/extern/old-work/needle-20060731-0718033686657.output

```

```

#
# Aligned sequences: 2
# 1: SEQ175
# 2: B_weihenstephensis
# Matrix: SELOSSUM62
# Gap penalty: 10.0
# Extend penalty: 0.5
#
# Length: 525
# Identity: 334/525 (63.6%)
# Similarity: 334/525 (63.6%)
# Gaps: 36/525 (6.9%)
# Score: 1725.0
#

```

```

SEQ175      1 atgattaaccgcgctcattttggtcggcagggttaacgagagacccgagtt      50
B_weihensteph 1 ttgatgaatcgtggttatcctcgttggctggtttaactaaggaccctgactt      50

SEQ175      51 gcgttacactccaaagcgaggtggctgttgccacgtttacgtcgcggtca      100
B_weihensteph 51 acgttacacgcccgaatggtgttcagtagctactttttagctagctgtga      100

SEQ175      101 acgcctcgttttacaaatcagcagggcgagcgggaacgaggtttattattca      150
B_weihensteph 101 atcgcgcaatttgcgaatcaacaaggtgagcgtgaagctgactttattaat      150

SEQ175      151 tctgtcgtttggcgccgcagcgagggaacacgtgcccaacttttggaaaaa      200
B_weihensteph 151 tctgtcaatatggcgtaaacagcagaaaacgtggcaattatttggaaaaa      200

SEQ175      201 ggggagccttggctgggtgtgcatggccgactgcgaacccgcagctatgaaa      250
B_weihensteph 201 aggtagccttagcagcggttagcagcgactcttcaactcgttaattacgatg      250

SEQ175      251 atcaagaaggtcgcggtgtgtacgtgacgggaagtggcggtgatagcgctc      300
B_weihensteph 251 gcaagaagtggtaaacgtgtatatgtacaagaagttcttcggcgagagcgta      300

SEQ175      301 caatttcttgagcgcg---aaaggaaacgagcgagcagcgagg-----      338
B_weihensteph 301 caacttttagagccgcgctaatggcggtggggagcaacgtgggttcattcaa      350

SEQ175      339 --ggcga-cagcagggcgctactatggggatoca-----ttcccatcc      378
B_weihensteph 351 tcagcaacccatcagg-agctgggttcggtaaccgaagctcttaaccattc      399

SEQ175      379 gggcaagatc-agaaccaccaatatccgaacgaaaaaggggtttggcgcca      427
B_weihensteph 400 ggtca--atctagtaattcaggttaaccaaggttaacaggttaactccgga      447

```

SEQ175	428	t---cg---atgacgacccctttcgccaatgacggccagccgacgatat	470
B_weihensteph	445	tttacgaagaatgacacatccatttcgaatgttgggtcaaccgattgacat	497
SEQ175	471	ttctgatgatgatttgcggttt	492
B_weihensteph	498	ttcggacgacgatttaccattttaa	522

```
# Aligned_sequences: 2
# 1: SEQ175
# 2: B_subtilis
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5

# Length: 528
# Identity: 350/528 (66.3%)
# Similarity: 350/528 (66.3%)
# Gaps: 45/528 (8.5%)
# Score: 1860.0
```

10466-575.1

[illegible]

```

#####
# Program: needle
# Fundate: Mon Jul 31 07:21:22 2006
# Align_format: srspar
# Report_file: /ebi/extern/old-work/needle-20060731-07212194058950.output
#####

#-----
#
# Aligned_sequences: 2
# 1: SEQ175
# 2: B_halodurans
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 553
# Identity: 253/553 (45.8%)
# Similarity: 253/553 (45.8%)
# Gaps: 107/553 (19.3%)
# Score: 1074.0
#
#####

SEQ175      1      atgattaacgc-cgtc---attttgctcggaaggttaacg--ag      38
              |||...|||. || | | | | | | | | | | | | | |
B_halodurans 1      ttagaatggcaaatcatcatcggaatatcgattggcttgcacatttg      50

SEQ175      39      agatccggaggttgctggttacacatccaagcgaggtgg---ctggtgcac--      83
              ..|||...|||...|||...|||... ||||... |...|||
B_halodurans 51      caaacgggtctctctgagaaccac---cggattgacgtccggagccacca      97

SEQ175      84      -gtttacgctcgcggtca--accgtcggttacaaatcagcggcgagc      130
              -||...|||...|| | |||...|| | | | | | | | | |
B_halodurans 98      gattgttgcgcgaatcatcaccgccatt---gggttgtagggg-gagc      143

SEQ175      131     gggaaacggattttatccaatgtgtcgtttggcgccgcagcgcaaaac      180
              c||...||...|| | ||| | ||| | | | | | | | | | |
B_halodurans 144     cgccaccagaagtt--gtcaa-----cgtttgatccccccttgctttgtga      186

SEQ175      181     gtgcaccaacttttgaaaaaggggagcgttggtggtgctgagtcgcgact      230
              |...||...||...||... ||...|| | | | | | | | | |
B_halodurans 187     gccgcgcggttcaaggaatt-gaacgctt-tctg---ccatgacc-tct      229

SEQ175      231     g---caaacccgcagctatgaaaatcaagaaggtcg-----gcgtatg      270
              | | | | | | | | | | | | | | | | | | | | | | |
B_halodurans 230     gtccacaagactctgc---ggccttcattgtgtcataactgcgctgttg      276

SEQ175      271     tacgtgacgggaagtgggtgctgatag-cgtccaatttcttgagccgaaag      319
              -||...|| | | | | | | | | | | | | | | | | | |
B_halodurans 277     aatccgac--catcaaccacagctagactccctttt-----tcaata      318

SEQ175      320     gaacg-agcgagcagcagggggcgacag-caggcggctaac---tatgggg      364
              |... ||...||... ||...|| | | | | | | | | | |
B_halodurans 319     gttcgccactgtccgcg-ttgettccgccaacgac-acagttaatgaa      366

SEQ175      365     atc-----cattcccattcgggcaagatc-agaaccaccaatcoga      406
              || | | | | | | | | | | | | | | | | | | | |
B_halodurans 367     atctgcttcgcgctctcctt---gttggttcgagaacggcggtttacag      413

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SEQ175	407	acgaaaaagggtttg----gccgcacg-atgacgacgttttgcg--ca	448
B_halodurans	414	caagtgtaaagtttgctacagcaacacggtttggcgtg--tagcgcact	461
SEQ175	449	atg----acg-gccagcgcgacgatatttct--gatg--atgattgcgcg	489
B_halodurans	462	ctggatcacgtgtcaaccgacgca-----ctaggacgacagatttaaca	506
SEQ175	490	ttt	492
B_halodurans	507	t	507

Program: needle

RunDate: Mon Jul 31 07:22:20 2006

Align_format: ssepair

Report_file: /cbl/extserv/old-work/needle-20060731-07222012434590.output

##

##

Aligned sequences: 2

1: SEQ175

2: B_clausii

Matrix: ERIOSUM62

Gap_penalty: 10.0

Extend_penalty: 0.5

##

Length: 552

Identity: 257/552 (46.6%)

Similarity: 257/552 (46.6%)

Gaps: 126/552 (22.8%)

Score: 1055.5

##

##

```

SEQ175      1      at-gattaacgcgctc----attttggctcg-gcaggttaacgaga      39
              || ||..||..||| |||...|| |..|...|||
B_clausii    1 Ttaaagtgaagatcatcgctcggaatatcaatcgaaacgtcattcgaga      50
40 gatccggaagttgcgtta-cactccaagcggagtgctgttgccacgcttta      88
              ||| || ||| |||..||..||..|||...||| |||
B_clausii    51 ---acgg-gt--cgttatcatatccattagaacggctgcacaca-gttt--      92
89 cgtctgcggctc--aacgcgtcgcttacaatcagcagggcgagcgg---g      133
              |..|| | |||..| |..|| ||| |..||..| .
B_clausii    93 -ggttgc--cagaacott--ggttgc---cagc--gcgctactgatca      130
134 aaacggattttattcaatgtgctgtttggcgccgccag--gcggaaaacg      181
              |||...||| |||...|| |..||..||..| |||...
B_clausii    131 aaaccaggattattccagag--gattggtttgactgttgcgaggt---      175
182 tcgccnaacttttgaaaaaggaggagctt--ggctggtgtcgatggccgac      229
              |||..||..| |..||| |..|| |..||..||..|
B_clausii    176 tcgagaaatt-----ggacgctttcagc---aacgatttcgct-      210
230 tgcnaaacccgcagct-----atgaaaatcagaaggtcggcgtgtgtac      273
              |..||..||..|| |..||..|| |..||..||..|
B_clausii    211 tacaaaaacgcgctgccttcattattgtca--tagcttcgcttgccac      258
274 gtgacggaagt-ggtggtgatagcgtccaaattctctgagccgaaaggaa      322
              |||..|| |...|||..||..||..||..||..||..|
B_clausii    259 ---acggcgttcgactcctgcgaagctcctttttaaggaaattggcga      305
323 cgaagcg-agg-----agcgagggcgagaca-----gcaggcggctact      358
              ||..| || |..||..||..| |..||..||..|
B_clausii    306 cgttctcagcgggtttgcgcgcagacacacagttaatgaagtgcagcttct      355
359 atgggggatocattcccatcggggcaagatcagaacc--accaatato--c      404
              |..||..|| |..||..||..| |..||..||..|
B_clausii    356 -----cgttctcctt---gctggtttgaaaacgagcggttgactgc      393

```

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SEQ175      405 gaacgaaaaagggtttgggcgcgcgatcgatgacgat---cct--ttcgccaa      449
      .|.|||.|||.  |||||.|||.|||.|||.  |||.  |||||.
B_clausii  394 aagcgtaaaa---ttggctacagctacacogtttggcg'gaar'cgcaat      439

SEQ175      450 tgacgggcacgcgat---cgatatttctgatgatgatttgcggtt      492
      |||.|||.|||.|||.  |||.  |||.|||.|||.|||.|||.
B_clausii  440 tcagggtracgcggttaagcg-----tcgcacaagaacaacacgggtttaa      484

SEQ175      493          492

B_clausii  485 aa      486

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